

How to use the macros for the comparison of *MuKpi* macro with GEANT

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The current location of the code is at :
/star/institutions/emn/bouchet/Joe/
I use *STARPRO* version.

1 Brief introduction to the code

There are 3 macros to use in order to plot comparison (of p_T , decaylength,etc ...) of D^0 reconstructed by *MuKpi* and the initial input from GEANT :

- `geant_out_all.C`¹ : run over `.geant.root` file
- `myMuKpi.C` : run over `.MuDst.root` file
- `readHisto.C` : make histogram

The idea is to create histogram from the GEANT input, then from the MuDst input and combine them.

1.1 `geant_out_all.C`

the output file name is `myresults_geant.root`

you have to set the number of files to set ; there is a link in the macro to the D^0 pure sample list I used : `mypureD0listGeant2.list`.

We know that for each file, 400 D^0 are in, then I declare $400 \times N_{\text{File}}$ histograms for the p_T and decay length of D^0 :

1. : `hpTDOGEANT_CurrentFile` : it is a 1-D histogram with X-axis from 1 to 400 (number of event Id in this file). the Y-axis will have the value of the p_T of the D^0 (see figure 1)
2. : `hDecay_CurrentFile` : it is a 1-D histogram with X-axis from 1 to 400 (number of event Id in this file). the Y-axis will have the value of the decay length of the D^0

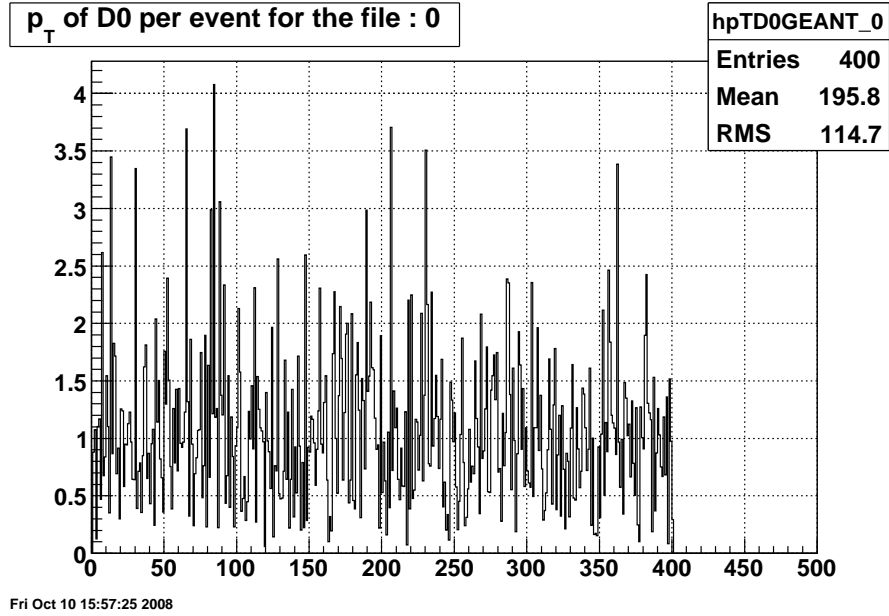


Figure 1: for a given file : X-axis : number of event ; Y-axis : the peak gives the value of the p_T of the D^0

There are not cut in this macro : we have to fill all the D^0 reconstructed : we select them by looping over the *g2t_Track_table* and by requiring that the GEANT_id of the current track is 37 and that the vertex id of this track has the same id of the vertex of the next tracks ($\text{stop_vertex_id}(i) = \text{start_vertex_id}(i+1)$).

The decay length is calculated as :

$$DL = \sqrt{\vec{L} \vec{L}} \quad (1)$$

where \vec{L} is a vector which components are :

$L_i = \text{SecondaryVertex}_i - \text{PrimaryVertex}_i$, with $i = \{x, y, z\}$

1.2 myMuKpi.C

This macro is the same as we used previously, so it has some cuts related to event position, quality of tracks.

The same histogram as in *geant_out_all.C* are also filled in this macro ; their names are :

1. *hpTD0_CurrentFile*
2. *hdLD0_CurrentFile*

The p_T is calculated as :

$$p_T = PP[s].Perp(); \quad (2)$$

¹the name of output and macro don't make any differences : you can recall them as you want

,where PP is the TLorentzVector from the association of positive and negative tracks.

DL is calculated as :

$$DL = \sqrt{diff_x^2 + diff_y^2 + diff_z^2} \quad (3)$$

, where $diff_i = dl_i - PrimaryVertex_i$ with dl (0-field approximation) from DCA_xy and DCA_z of daughter tracks.

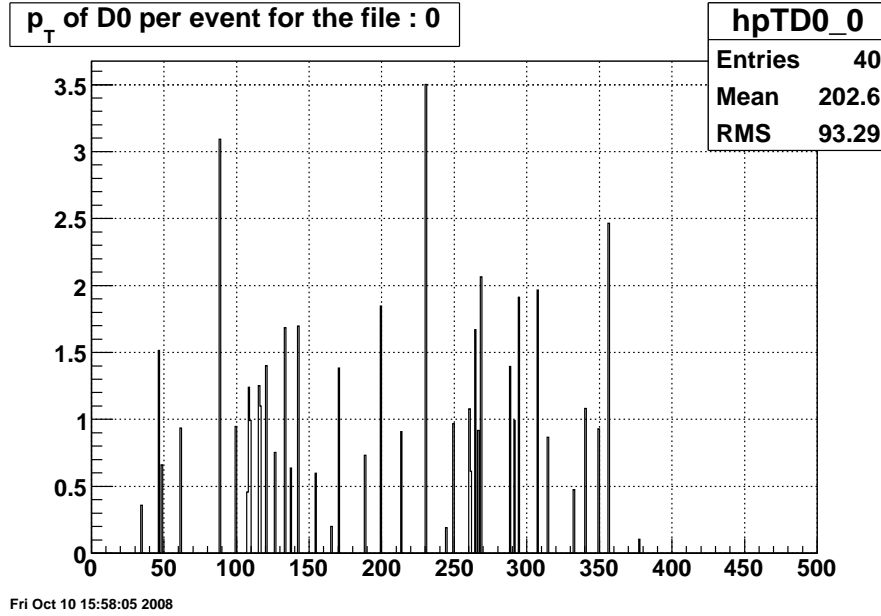


Figure 2: for a given file : X-axis : number of event ; Y-axis : the peak gives the value of the p_T of the D^0

From Fig. 2, we see that the number of entries (for the same file) is much lower than in GEANT ; it is because of the cuts apply in the macro that removes some events

1.3 readHisto.C

The last part is to make association : this macro opens the 2 root files where histograms are written.

For each file processed :

1. retrieve the proper histogram from the first root file
2. loop over the bin x (event Id) and get the p_T value
3. for the current bin, open the second root file and get the same p_T if it exists
4. fill some histograms

The histograms write the difference $p_T^{GEANT} - p_T^{MuKpi}$ as a function of p_T^{GEANT} in order to use *FitSlicesY()* from *ROOT* to plot the mean and σ .

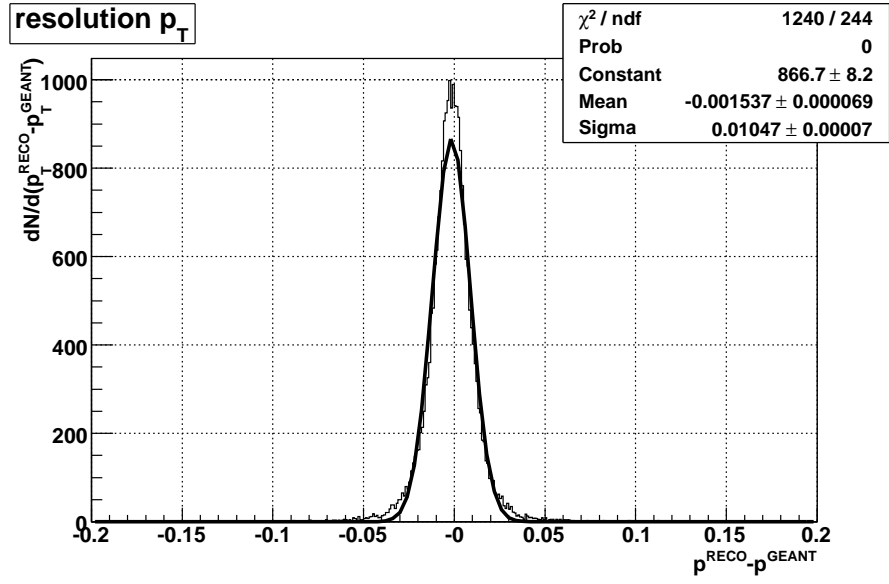


Figure 3: Distribution of $p_T^{\text{GEANT}} - p_T^{\text{MuKpi}}$

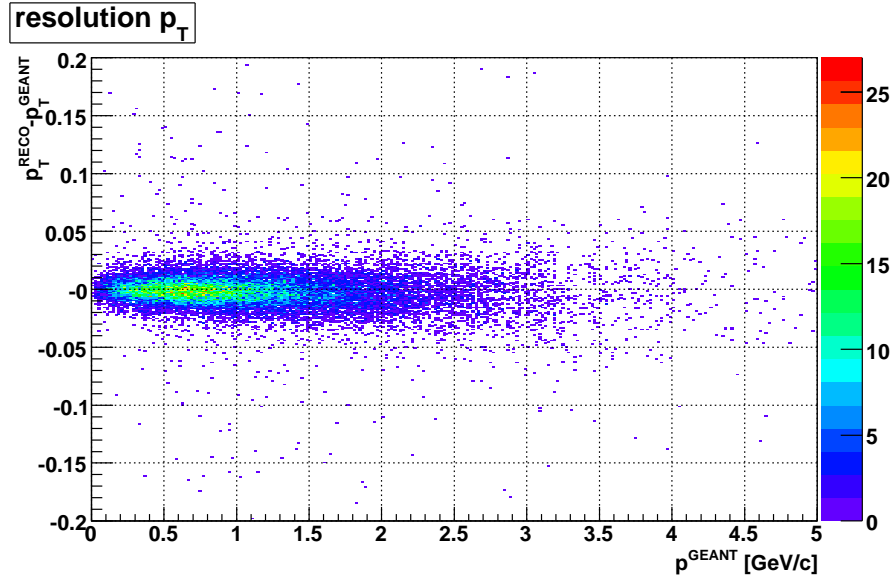
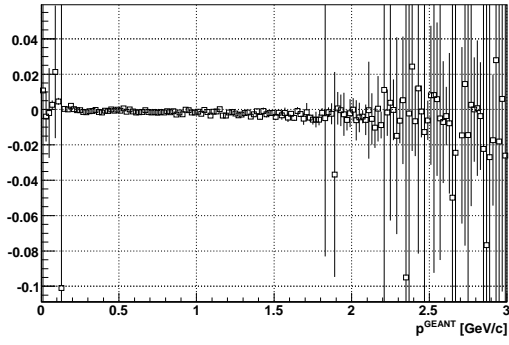


Figure 4: Distribution of $p_T^{\text{GEANT}} - p_T^{\text{MuKpi}}$ vs p_T^{GEANT}

The next histograms are the results from *FitSlicesY()*

Fitted value of par[1]=Mean



Fitted value of par[2]=Sigma

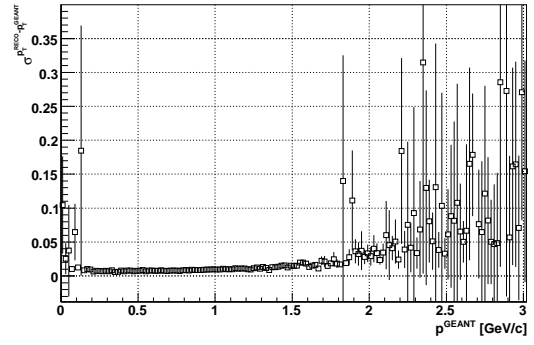


Figure 5: Mean and σ of Δp_t